

copy

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Caras, Ingrid W
- (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/635130
 - (B) FILING DATE: 19-Mar-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Torchia, PhD., Timothy E.
 - (B) REGISTRATION NUMBER: 36,700
 - (C) REFERENCE/DOCKET NUMBER: P1001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-8674
 - (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1877 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ix) FEATURE:
 - (A) NAME/KEY: Extra Cellular Domain
 - (B) LOCATION: 244-899
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GNTCTAGAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCT 50
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGGCGGG GTC ATG 246
                                     Met
                                     1

GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
                    5                      10

GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
    15                      20                      25

CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
        30                      35                      40

AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
        45                      50

ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
    55                      60                      65

CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
        70                      75
```

AAG	CTG	TAC	CTG	GTA	GGG	GGT	GCT	CAG	GGC	CGG	CGC	TGT	519
Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	Arg	Cys	
80					85					90			
GAG	GCA	CCC	CCT	GCC	CCA	AAC	CTC	CTT	CTC	ACT	TGT	GAT	558
Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
		95					100					105	
CGC	CCA	GAC	CTG	GAT	CTC	CGC	TTC	ACC	ATC	AAG	TTC	CAG	597
Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	
				110					115				
GAG	TAT	AGC	CCT	AAT	CTC	TGG	GGC	CAC	GAG	TTC	CGC	TCG	636
Glu	Tyr	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	
	120					125					130		
CAC	CAC	GAT	TAC	TAC	ATC	ATT	GCC	ACA	TCG	GAT	GGG	ACC	675
His	His	Asp	Tyr	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	
			135					140					
CGG	GAG	GGC	CTG	GAG	AGC	CTG	CAG	GGA	GGT	GTG	TGC	CTA	714
Arg	Glu	Gly	Leu	Glu	Ser	Leu	Gln	Gly	Gly	Val	Cys	Leu	
145					150					155			
ACC	AGA	GGC	ATG	AAG	GTG	CTT	CTC	CGA	GTG	GGA	CAA	AGT	753
Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	Arg	Val	Gly	Gln	Ser	
		160					165					170	
CCC	CGA	GGA	GGG	GCT	GTC	CCC	CGA	AAA	CCT	GTG	TCT	GAA	792
Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	Val	Ser	Glu	
				175						180			
ATG	CCC	ATG	GAA	AGA	GAC	CGA	GGG	GCA	GCC	CAC	AGC	CTG	831
Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	Leu	
	185					190					195		
GAG	CCT	GGG	AAG	GAG	AAC	CTG	CCA	GGT	GAC	CCC	ACC	AGC	870
Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	
			200					205					
AAT	GCA	ACC	TCC	CGG	GGT	GCT	GAA	GGC	CCC	CTG	CCC	CCT	909
Asn	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	
210					215					220			
CCC	AGC	ATG	CCT	GCA	GTG	GCT	GGG	GCA	GCA	GGG	GGG	CTG	948
Pro	Ser	Met	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	
		225					230					235	
GCG	CTG	CTC	TTG	CTG	GGC	GTG	GCA	GGG	GCT	GGG	GGT	GCC	987
Ala	Leu	Leu	Leu	Leu	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	

240

245

ATG	TGT	TGG	CGG	AGA	CGG	CGG	GCC	AAG	CCT	TCG	GAG	AGT	1026
Met	Cys	Trp	Arg	Arg	Arg	Arg	Ala	Lys	Pro	Ser	Glu	Ser	
	250					255					260		

CGC	CAC	CCT	GGT	CCT	GGC	TCC	TTC	GGG	AGG	GGA	GGG	TCT	1065
Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	Arg	Gly	Gly	Ser	
			265					270					

CTG	GGC	CTG	GGG	GGT	GGA	GGT	GGG	ATG	GGA	CCT	CGG	GAG	1104
Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	Arg	Glu	
275					280					285			

GCT	GAG	CCT	GGG	GAG	CTA	GGG	ATA	GCT	CTG	CGG	GGT	GGC	1143
Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
		290					295					300	

GGG	GCT	GCA	GAT	CCC	CCC	TTC	TGC	CCC	CAC	TAT	GAG	AAG	1182
Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	
				305					310				

GTG	AGT	GGT	GAC	TAT	GGG	CAT	CCT	GTG	TAT	ATC	GTG	CAG	1221
Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	
	315					320					325		

GAT	GGG	CCC	CCC	CAG	AGC	CCT	CCA	AAC	ATC	TAC	TAC	ACA	1260
Asp	Gly	Pro	Pro	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	
			330					335					

TCG	ATT	TCT	GTG	TTG	GAG	TGG	CCC	ATA	TTG	CAT	ACG	ATA	1299
Ser	Ile	Ser	Val	Leu	Glu	Trp	Pro	Ile	Leu	His	Thr	Ile	
340					345					350			

CAA	CTG	TTT	TTC	ATG	CGA	TCC	AAG	TGC	TCC	CGT	GTC	ACT	1338
Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	Cys	Ser	Arg	Val	Thr	
		355					360					365	

ACA	TTC	TTA	TTT	CCT	GTG	CAA	GTT	ATT	ACG	ACA	TCG	ACT	1377
Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	Thr	Ser	Thr	
				370					375				

TGC	CGG	ATG	ACT	TCA	TTT	AGC	TTT	ACC	ACC	CTG	AAC	CCA	1416
Cys	Arg	Met	Thr	Ser	Phe	Ser	Phe	Thr	Thr	Leu	Asn	Pro	
	380					385					390		

TCC	ATG	CAG	GCC	TGC	AGA	GCA	CAG	ATG	GGG	GAA	TTC	CGA	1455
Ser	Met	Gln	Ala	Cys	Arg	Ala	Gln	Met	Gly	Glu	Phe	Arg	
			395					400					

ATC	AGA	TGG	TGT	TTC	TGG	GGG	GAC	AGG	ATC	CTG	GGT	ACG	1494
Ile	Arg	Trp	Cys	Phe	Trp	Gly	Asp	Arg	Ile	Leu	Gly	Thr	
405					410					415			

GCT	CTG	TTT	GTG	CTT	GTG	CTT	ATT	CTT	CTT	CTT	GGG	AGG	1533
Ala	Leu	Phe	Val	Leu	Val	Leu	Ile	Leu	Leu	Leu	Gly	Arg	
	420					425					430		

CTG	AAT	ATG	CAT	CAG	ACG	ACA	CTG	CTC	CGG	CAA	CGG	GCC	1572
Leu	Asn	Met	His	Gln	Thr	Thr	Leu	Leu	Arg	Gln	Arg	Ala	
				435					440				

AGT	GTG	GAG	GCG	GAA	GCC	GGC	CAG	CAT	GGT	CCC	CTG	TG	1610
Ser	Val	Glu	Ala	Glu	Ala	Gly	Gln	His	Gly	Pro	Leu		
	445					450					455		

ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660

GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710

CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760

TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810

CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTCGA TATCAAGCTT 1860

ATCGATACCG TCGACCT 1877

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Pro	Pro	His	Ser	Gly	Pro	Gly	Gly	Val	Arg	Val	Gly	Ala
1				5					10					15

Leu	Leu	Leu	Leu	Gly	Val	Leu	Gly	Leu	Val	Ser	Gly	Leu	Ser	Leu
				20					25					30

Glu	Pro	Val	Tyr	Trp	Asn	Ser	Ala	Asn	Lys	Arg	Phe	Gln	Ala	Glu
				35					40					45

Gly	Gly	Tyr	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Arg	Leu	Asp	Leu
				50					55					60

Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn

				65					70					75	
Tyr	Glu	Phe	Tyr	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	
				80					85					90	
Arg	Cys	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
				95					100					105	
Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
				110					115					120	
Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
				125					130					135	
Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
				140					145					150	
Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
				155					160					165	
Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
				170					175					180	
Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
				185					190					195	
Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
				200					205					210	
Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
				215					220					225	
Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
				230					235					240	
Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
				245					250					255	
Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
				260					265					270	
Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
				275					280					285	
Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
				290					295					300	
Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
				305					310					315	

Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	320	325	330
Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	Ser	Ile	Ser	Val	Leu	Glu	335	340	345
Trp	Pro	Ile	Leu	His	Thr	Ile	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	350	355	360
Cys	Ser	Arg	Val	Thr	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	365	370	375
Thr	Ser	Thr	Cys	Arg	Met	Thr	Ser	Phe	Ser	Phe	Thr	Thr	Leu	Asn	380	385	390
Pro	Ser	Met	Gln	Ala	Cys	Arg	Ala	Gln	Met	Gly	Glu	Phe	Arg	Ile	395	400	405
Arg	Trp	Cys	Phe	Trp	Gly	Asp	Arg	Ile	Leu	Gly	Thr	Ala	Leu	Phe	410	415	420
Val	Leu	Val	Leu	Ile	Leu	Leu	Leu	Gly	Arg	Leu	Asn	Met	His	Gln	425	430	435
Thr	Thr	Leu	Leu	Arg	Gln	Arg	Ala	Ser	Val	Glu	Ala	Glu	Ala	Gly	440	445	450
Gln	His	Gly	Pro	Leu											455		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GNTCTAGAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCT 50
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTCATGGGGC 250

```

CCCCCCATTC TGGGCCGGGG GGC GTGCGAG TCGGGGCCCT GCTGCTGCTG 300
 GGGGTTTTGG GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350
 CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC 400
 AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCCG GCCTCCTGGC 450
 CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500
 TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA 550
 CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600
 TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650
 CATCAT TGCC ACATCGGATG GGACCCGGGA GGCCTGGAG AGCCTGCAGG 700
 GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750
 AGTCCCCGAG GAGGGGCTGT CCCCCGAAAA CCTGTGTCTG AAATGCCCAT 800
 GGAAAGAGAC CGAGGGGCAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC 850
 TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900
 CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950
 GCTGCTCTTG CTGGGCGTGG CAGGGGCTGG GGGTGCCATG TGTTGGCGGA 1000
 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC 1050
 GGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG 1100
 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGT GGCGGGGCTG 1150
 CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGA CTATGGG 1200
 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT 1250
 CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC 1300
 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA 1350
 ACATCTCGGC CCCCTGTGCC CCCCAGCCC CTTCACTCCT CCCGGCTGCT 1400
 GTCCTCGTCT CCACTTTTAG GATTCCTTAG GATTCCCACT GCCCACTTC 1450
 CTGCCCTCCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG 1500

ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550
 ACCCAGGCAT CCTTGTC CCC CTCACCCACC CAGAGCTAGG GGCGGGAACA 1600
 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT 1650
 CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700
 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT 1750
 ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTTCTCCC 1800
 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850
 TCTGCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCCAG 1900
 CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950
 ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000
 AGAAGAAGTG TCCCGTTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050
 TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGGCCA CTTGGGACCG 2100
 GAAGTGACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150
 TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCATCCAG 2200
 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA 2250
 GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300
 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACCT 2350
 ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Pro	Pro	His	Ser	Gly	Pro	Gly	Gly	Val	Arg	Val	Gly	Ala
1				5					10					15
Leu	Leu	Leu	Leu	Gly	Val	Leu	Gly	Leu	Val	Ser	Gly	Leu	Ser	Leu
				20					25					30

Glu	Pro	Val	Tyr	Trp	Asn	Ser	Ala	Asn	Lys	Arg	Phe	Gln	Ala	Glu	35	40	45
Gly	Gly	Tyr	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Arg	Leu	Asp	Leu	50	55	60
Leu	Cys	Pro	Arg	Ala	Arg	Pro	Pro	Gly	Pro	His	Ser	Ser	Pro	Asn	65	70	75
Tyr	Glu	Phe	Tyr	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	80	85	90
Arg	Cys	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	95	100	105
Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	110	115	120
Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	125	130	135
Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	140	145	150
Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	155	160	165
Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	170	175	180
Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	185	190	195
Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	200	205	210
Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	215	220	225
Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	230	235	240
Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	245	250	255
Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	260	265	270
Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	275	280	285

Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	290	295	300
Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	305	310	315
Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	320	325	330
Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Lys	Val						335	340	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCGACGCTG TGAGGCACCC CCTGCCCCAA ACCTCCTTCT CACTTGTGAT 50
 CGCCCAGACC TGGATCTCCG CTTCAACCATC AAGTTCCAGG AGTATAGCCC 100
 TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTG 150
 CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG 200
 TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA 250
 GGAGGGGCTG TCCCCGAAA ACCTGTGTCT GAAATGCCCA TGGAAAGAGA 300
 CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG 350
 TGACCCACCC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400
 CCCTTTCCCA GCATTGCNTG CANTTGGTTN GGGGCAGCAN GGGGGNGTTT 450
 TGGC 454

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50
CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50
TTCCATGGGC 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala
1 5 10 15
Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys
20 25 30

Asn	Leu	Glu	Pro	Val	Ser	Trp	Ser	Ser	Leu	Asn	Pro	Lys	Phe	Leu	35	40	45
Ser	Gly	Lys	Gly	Leu	Val	Ile	Tyr	Pro	Lys	Ile	Gly	Asp	Lys	Leu	50	55	60
Asp	Ile	Ile	Cys	Pro	Arg	Ala	Glu	Ala	Gly	Arg	Pro	Tyr	Glu	Tyr	65	70	75
Tyr	Lys	Leu	Tyr	Leu	Val	Arg	Pro	Glu	Gln	Ala	Ala	Ala	Cys	Ser	80	85	90
Thr	Val	Leu	Asp	Pro	Asn	Val	Leu	Val	Thr	Cys	Asn	Arg	Pro	Glu	95	100	105
Gln	Glu	Ile	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Phe	Ser	Pro	Asn	110	115	120
Tyr	Met	Gly	Leu	Glu	Phe	Lys	Lys	His	His	Asp	Tyr	Tyr	Ile	Thr	125	130	135
Ser	Thr	Ser	Asn	Gly	Ser	Leu	Glu	Gly	Leu	Glu	Asn	Arg	Glu	Gly	140	145	150
Gly	Val	Cys	Arg	Thr	Arg	Thr	Met	Lys	Ile	Ile	Met	Lys	Val	Gly	155	160	165
Gln	Asp	Pro	Asn	Ala	Val	Thr	Pro	Glu	Gln	Leu	Thr	Thr	Ser	Arg	170	175	180
Pro	Ser	Lys	Glu	Ala	Asp	Asn	Thr	Val	Lys	Met	Ala	Thr	Gln	Ala	185	190	195
Pro	Gly	Ser	Arg	Gly	Ser	Leu	Gly	Asp	Ser	Asp	Gly	Lys	His	Glu	200	205	210
Thr	Val	Asn	Gln	Glu	Glu	Lys	Ser	Gly	Pro	Gly	Ala	Ser	Gly	Gly	215	220	225
Ser	Ser	Gly	Asp	Pro	Asp	Gly	Phe	Phe	Asn	Ser	Lys	Val	Ala	Leu	230	235	240
Phe	Ala	Ala	Val	Gly	Ala	Gly	Cys	Val	Ile	Phe	Leu	Leu	Ile	Ile	245	250	255
Ile	Phe	Leu	Thr	Val	Leu	Leu	Leu	Lys	Leu	Arg	Lys	Arg	His	Arg	260	265	270
Lys	His	Thr	Gln	Gln	Arg	Ala	Ala	Ala	Leu	Ser	Leu	Ser	Thr	Leu	275	280	285

Ala	Ser	Pro	Lys	Gly	Gly	Ser	Gly	Thr	Ala	Gly	Thr	Glu	Pro	Ser
				290					295					300
Asp	Ile	Ile	Ile	Pro	Leu	Arg	Thr	Thr	Glu	Asn	Asn	Tyr	Cys	Pro
				305					310					315
His	Tyr	Glu	Lys	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile
				320					325					330
Val	Gln	Glu	Met	Pro	Pro	Gln	Ser	Pro	Ala	Asn	Ile	Tyr	Tyr	Lys
				335					340					345
Val														
346														

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Val	Arg	Arg	Asp	Ser	Val	Trp	Lys	Tyr	Cys	Trp	Gly	Val
1				5					10					15
Leu	Met	Val	Leu	Cys	Arg	Thr	Ala	Ile	Ser	Lys	Ser	Ile	Val	Leu
				20					25					30
Glu	Pro	Ile	Tyr	Trp	Asn	Ser	Ser	Asn	Ser	Lys	Phe	Leu	Pro	Gly
				35					40					45
Gln	Gly	Leu	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Lys	Leu	Asp	Ile
				50					55					60
Ile	Cys	Pro	Lys	Val	Asp	Ser	Lys	Thr	Val	Gly	Gln	Tyr	Glu	Tyr
				65					70					75
Tyr	Lys	Val	Tyr	Met	Val	Asp	Lys	Asp	Gln	Ala	Asp	Arg	Cys	Thr
				80					85					90
Ile	Lys	Lys	Glu	Asn	Thr	Pro	Leu	Leu	Asn	Cys	Ala	Lys	Pro	Asp
				95					100					105
Gln	Asp	Ile	Lys	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Phe	Ser	Pro	Asn
				110					115					120
Leu	Trp	Gly	Leu	Glu	Phe	Gln	Lys	Asn	Lys	Asp	Tyr	Tyr	Ile	Ile
				125					130					135

Ser	Thr	Ser	Asn	Gly	Ser	Leu	Glu	Gly	Leu	Asp	Asn	Gln	Glu	Gly	140	145	150
Gly	Val	Cys	Gln	Thr	Arg	Ala	Met	Lys	Ile	Leu	Met	Lys	Val	Gly	155	160	165
Gln	Asp	Ala	Ser	Ser	Ala	Gly	Ser	Thr	Arg	Asn	Lys	Asp	Pro	Thr	170	175	180
Arg	Arg	Pro	Glu	Leu	Glu	Ala	Gly	Thr	Asn	Gly	Arg	Ser	Ser	Thr	185	190	195
Thr	Ser	Pro	Phe	Val	Lys	Pro	Asn	Pro	Gly	Ser	Ser	Thr	Asp	Gly	200	205	210
Asn	Ser	Ala	Gly	His	Ser	Gly	Asn	Asn	Ile	Leu	Gly	Ser	Glu	Val	215	220	225
Ala	Leu	Phe	Ala	Gly	Ile	Ala	Ser	Gly	Cys	Ile	Ile	Phe	Ile	Val	230	235	240
Ile	Ile	Ile	Thr	Leu	Val	Val	Leu	Leu	Leu	Lys	Tyr	Arg	Arg	Arg	245	250	255
His	Arg	Lys	His	Ser	Pro	Gln	His	Thr	Thr	Thr	Leu	Ser	Leu	Ser	260	265	270
Thr	Leu	Ala	Thr	Pro	Lys	Arg	Ser	Gly	Asn	Asn	Asn	Gly	Ser	Glu	275	280	285
Pro	Ser	Asp	Ile	Ile	Ile	Pro	Leu	Arg	Thr	Ala	Asp	Ser	Val	Phe	290	295	300
Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	305	310	315
Tyr	Ile	Val	Gln	Glu	Met	Pro	Pro	Gln	Ser	Pro	Ala	Asn	Ile	Tyr	320	325	330
Tyr	Lys	Val													333		